

REMARKS

Claims 33-37, 39, 40 and 52-55 were pending prior to entering the amendments.

The Amendment

SEQ ID NOs: 1-14 are inserted at the end of the specification. These sequences are identical to those sequences submitted in the paper copy and computer-readable format of the sequence listing on July 18, 2007. Applicants submit that the material being inserted is the material previously incorporated by reference and that the amendment contains no new matter (37CFR 1.57(f)).

Claim 33 is amended to recite high grade cervical intraepithelial neoplasia; support for the amendment can be found, for example, page 40, line 5. Claim 33 is also amended to recite that threshold levels of the normalization markers is determined from an adequate and predefined amount of ectocervical cells or endocervical cells; support for the amendment can be found, for example, at page 47, lines 6-19. Claim 33 is further amended to clarify the meaning of the claim. Support for the amendment can be found, for example, at page 47, lines 1-26.

Claim 40 is amended to correct the typographic error of endocervical to ectocervical. Support for the amendment can be found at page 30, lines 5-8 and Table 1.

New Claim 56 is similar to Claim 33 except that it recites determining the presence or absence of a detectable level of at least one normalization marker. Support for the amendment can be found at page 20, lines 24-27.

New Claims 57-62 are similar to Claims 36, 37, 39, 40, 54, and 55.

No new matter is added in any of the amendments. The Examiner is requested to enter the amendment and reconsider the application.

The Response

Objection to Amendment

4. Applicants have amended the specification to insert SEQ ID NOs: 1-14. Applicants submit that the material being inserted is the material previously incorporated by reference and that the amendment contains no new matter (37CFR 1.57(f)).

Objection to the Specification

5. Applicant have properly identified the trademark of HYBOND®.

35 USC §112 Second Paragraph Rejection

7. Claims 33-37, 39, 40 and 52-55 are rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The Examiner states that it cannot be ascertained how the determination that the sample is adequate, or not, is made by the comparison step; and furthermore, it cannot be ascertained how cervical dysplasia, cervical cancer or cervical intraepithelial neoplasia is detected upon the "basis" of the level of and the adequacy of the sample.

Applicants have amended Claim 33 to recite that threshold levels of the normalization markers is determined from an adequate and predefined amount of ectocervical cells or endocervical cells. At page 47 at lines 9-17, the application describes how to determine a threshold value by measuring the OD value of an adequate and predefined amount of endocervical cells or ectocervical cells. Although the application exemplifies 200,000 squamous ectocervical cells, 2000 columnar endocervical cells and the OD values, it must be understood that the value for the cells as well for OD may vary depending to the reaction conditions. Those of skill in the art know how an appropriate threshold value for a particular test format may be established.

Therefore, the §112 second paragraph rejection should be withdrawn in view of the claim amendment.

35 USC §112 First Paragraph Rejection

9. Claims 33-37, 39, 40 and 52-55 are rejected under 35 U.S.C. §112, first paragraph, as allegedly failing to comply with the written description requirement.

The Examiner states that none of the claims are directed to both a particularly identified "relevant marker" and a particularly identified "normalization marker".

Applicants have amended Claim 33 to identify the relevant marker as p16^{INK4a} and the normalization markers as proteins having SEQ ID NOs:1-12.

10. Claims 33-37, 39, 40 and 52-55 are rejected under 35 U.S.C. §112, first paragraph, because the specification, while being enabling for using a process for diagnosing cervical dysplasia or cervical cancer, said process comprising detecting the level of expression p16^{INK4a}, does not allegedly provide enablement for using a process for diagnosing any type of cervical intraepithelial neoplasia.

Applicants have amended Claim 33 to recite detecting high grade cervical intraepithelial neoplasia.

The Examiner states that a marker that does not distinguish cervical dysplasia, cervical cancer, and cervical intraepithelial neoplasia cannot be expected to be useful in the differential diagnosis of such conditions or diseases.

Applicants respectfully submit that the claims are directed to a method for detecting cervical dysplasia, cervical cancer, or high grade cervical intraepithelial neoplasia, which is a screening method, and is not a method for differential diagnosis.

The Examiner states that the values of the "threshold levels" of the normalization markers to which the claims refer are not known or disclosed.

Applicants have amended the claim to recite how to determine the threshold levels.

35 USC §112 Second Paragraph Rejection

11. Claims 33-37, 39, 40 and 52-55 are rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Applicants have amended the claims to address the issues.

35 USC §112 First Paragraph Rejection

Claims 33-37, 39, 40 and 52-55 are rejected under 35 U.S.C. §112, first paragraph, as allegedly failing to comply with the written description requirement.

Gamma-Catenin, Ep-Cam, E-Cadherin, alpha-1 Catenin, alpha-2 Catenin, beta-Catenin, Involucrin, and p120 are identified in Table 1 by accession numbers. Cytokeratin 8, 18, 10, and 13, p16^{INK4a} and p14ARF are known proteins with well-established sequences. Those skilled in the art would know the exact sequence cytokeatin 8, 18, 10, and 13, p16^{INK4a} and p14ARF. In the Response submitted on July 18, 2007, Applicants have already provided NCBI sequences of the above proteins; each sequence is identified by its name and accession number.

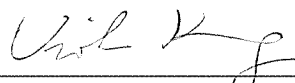
Applicants have amended the specification to insert SEQ ID NOs: 1-14. Applicants submit that the material being inserted is the material previously incorporated by reference and that the amendment contains no new matter (37CFR 1.57(f)).

Conclusion

For all the foregoing reasons, reconsideration of and withdrawal of all outstanding rejections is respectfully requested. The Examiner is earnestly solicited to allow all claims, and pass this application to issuance.

Respectfully submitted,

Date: October 30, 2007



Viola T. Kung, Ph.D. (Reg. No. 41,131)

Enclose: Paper copy of Sequence Listing

HOWREY LLP
2941 Fairview Park Drive, **Box No. 7**
Falls Church, VA 22042
Telephone No. (650) 798-3570
Facsimile No. (650) 798-3600

SEQUENCE LISTING

<110> Rudiger Ridder, et.al.
 <120> Method for solution based diagnosis
 <130> 05033.0003.00US00
 <140> 10/633,484
 <141> 2003-07-31
 <150> EP 02017313.4
 <151> 2002-08-01
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Cys Gly Arg Gln Tyr Thr Leu Lys Lys Thr Thr Thr Tyr Thr Gln Gly
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 100 105 110

Leu Gln Arg Leu Ala Glu Pro Ser Gln Leu Leu Lys Ser Ala Ile Val
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His Leu Ile Asn Tyr Gln Asp Asp Ala Glu Leu Ala Thr Arg Ala Leu
 Page 1

130

135

140

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Lys Ala Ala Met Ile Val Asn Gln Leu Ser Lys Lys Glu Ala Ser Arg
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Arg Ala Leu Met Gly Ser Pro Gln Leu Val Ala Ala Val Val Arg Thr
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Met Gln Asn Thr Ser Asp Leu Asp Thr Ala Arg Cys Thr Thr Ser Ile
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Asn Tyr Ser Tyr Glu Lys Leu Leu Trp Thr Thr Ser Arg Val Leu Lys
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Gly Met Gln Ala Leu Gly Lys His Leu Thr Ser Asn Ser Pro Arg Leu
355 360 365

Val Gln Asn Cys Leu Trp Thr Leu Arg Asn Leu Ser Asp Val Ala Thr
370 375 380

Lys Gln Glu Gly Leu Glu Ser Val Leu Lys Ile Leu Val Asn Gln Leu
Page 2

385 390 395 400

Ser Val Asp Asp Val Asn Val Leu Thr Cys Ala Thr Gly Thr Leu Ser
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Asn Leu Thr Cys Asn Asn Ser Lys Asn Lys Thr Leu Val Thr Gln Asn
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Cys Glu Leu Ala Gln Asp Lys Glu Ala Ala Asp Ala Ile Asp Ala Glu
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Page 3

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Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
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His Phe Leu Val Tyr Ala Trp Asp Ser Thr Tyr Arg Lys Phe Ser Thr
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Gly Ser Arg Met Asp Lys Leu Gly Arg Thr Ile Ala Asp His Cys Pro
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Asp Ser Ala Cys Lys Gln Asp Leu Leu Ala Tyr Leu Gln Arg Ile Ala
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Leu Tyr Cys His Gln Leu Asn Ile Cys Ser Lys Val Lys Ala Glu Val
785 790 795 800

Gln Asn Leu Gly Gly Glu Leu Val Val Ser Gly Val Asp Ser Ala Met
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Ser Leu Ile Gln Ala Ala Lys Asn Leu Met Asn Ala Val Val Gln Thr
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Val Lys Ala Ser Tyr Val Ala Ser Thr Lys Tyr Gln Lys Ser Gln Gly
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Met Ala Ser Leu Asn Leu Pro Ala Val Ser Trp Lys Met Lys Ala Pro
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Glu Lys Lys Pro Leu Val Lys Arg Glu Lys Gln Asp Glu Thr Gln Thr
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Lys Lys Lys Gly Arg Ser Lys Lys Ala His Val Leu Ala Ala Ser Val
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Glu Gln Ala Thr Gln Asn Phe Leu Glu Lys Gly Glu Gln Ile Ala Lys
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Glu Ser Gln Asp Leu Lys Glu Glu Leu Val Ala Ala Val Glu Asp Val
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Asp Pro Cys Ser Ser Val Lys Arg Gly Thr Met Val Arg Ala Ala Arg
Page 13

115	120	125
Ala Leu Leu Ser Ala Val Thr Arg Leu Leu Ile Leu Ala Asp Met Ala	130	135
Asp Val Met Arg Leu Leu Ser His Leu Lys Ile Val Glu Glu Ala Leu	145	150
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Lys Glu Phe Gly Lys Glu Met Val Lys Leu Asn Tyr Val Ala Ala Arg	180	185
Arg Gln Gln Glu Leu Lys Asp Pro His Cys Arg Asp Glu Met Ala Ala	195	200
Ala Arg Gly Ala Leu Lys Lys Asn Ala Thr Met Leu Tyr Thr Ala Ser	210	215
Gln Ala Phe Leu Arg His Pro Asp Val Ala Ala Thr Arg Ala Asn Arg	225	230
Asp Tyr Val Phe Lys Gln Val Gln Glu Ala Ile Ala Gly Ile Ser Asn	245	250
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Ile Gly Glu Leu Ala Ala Ala Leu Asn Glu Phe Asp Asn Lys Ile Ile	275	280
Leu Asp Pro Met Thr Phe Ser Glu Ala Arg Phe Arg Pro Ser Leu Glu	290	295
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370

375

380

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Ser Glu Asn His Ile Leu Glu Asp Val Asn Lys Cys Val Ile Ala Leu
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Gln Glu Gly Asp Val Asp Thr Leu Asp Arg Thr Ala Gly Ala Ile Arg
 530 535 540

Gly Arg Ala Ala Arg Val Ile His Ile Ile Asn Ala Glu Met Glu Asn
 545 550 555 560

Tyr Glu Ala Gly Val Tyr Thr Glu Lys Val Leu Glu Ala Thr Lys Leu
 565 570 575

Leu Ser Glu Thr Val Met Pro Arg Phe Ala Glu Gln Val Glu Val Ala
 580 585 590

Ile Glu Ala Leu Ser Ala Asn Val Pro Gln Pro Phe Glu Glu Asn Glu
 595 600 605

Phe Ile Asp Ala Ser Arg Leu Val Tyr Asp Gly Val Arg Asp Ile Arg
 610 615 620

Lys Ala Val Leu Met Ile Arg Thr Pro Glu Glu Leu Glu Asp Asp Ser
 Page 15

625		630		635		640									
Asp	Phe	Glu	Gln	Glu	Asp	Tyr	Asp	Val	Arg	Ser	Arg	Thr	Ser	Val	Gln
				645					650					655	
Thr	Glu	Asp	Asp	Gln	Leu	Ile	Ala	Gly	Gln	Ser	Ala	Arg	Ala	Ile	Met
			660					665					670		
Ala	Gln	Leu	Pro	Gln	Glu	Glu	Lys	Ala	Lys	Ile	Ala	Glu	Gln	Val	Glu
		675					680					685			
Ile	Phe	His	Gln	Glu	Lys	Ser	Lys	Leu	Asp	Ala	Glu	Val	Ala	Lys	Trp
	690					695					700				
Asp	Asp	Ser	Gly	Asn	Asp	Ile	Ile	Val	Leu	Ala	Lys	Gln	Met	Cys	Met
705					710					715					720
Ile	Met	Met	Glu	Met	Thr	Asp	Phe	Thr	Arg	Gly	Lys	Gly	Pro	Leu	Lys
				725					730					735	
Asn	Thr	Ser	Asp	Val	Ile	Asn	Ala	Ala	Lys	Lys	Ile	Ala	Glu	Ala	Gly
			740					745					750		
Ser	Arg	Met	Asp	Lys	Leu	Ala	Arg	Ala	Val	Ala	Asp	Gln	Cys	Pro	Asp
		755					760					765			
Ser	Ala	Cys	Lys	Gln	Asp	Leu	Leu	Ala	Tyr	Leu	Gln	Arg	Ile	Ala	Leu
	770					775					780				
Tyr	Cys	His	Gln	Leu	Asn	Ile	Cys	Ser	Lys	Val	Lys	Ala	Glu	Val	Gln
785					790					795					800
Asn	Leu	Gly	Gly	Glu	Leu	Ile	Val	Ser	Gly	Thr	Gly	Val	Gln	Ser	Thr
				805					810					815	
Phe	Thr	Thr	Phe	Tyr	Glu	Val	Asp	Cys	Asp	Val	Ile	Asp	Gly	Gly	Arg
			820					825					830		
Ala	Ser	Gln	Leu	Ser	Thr	His	Leu	Pro	Thr	Cys	Ala	Glu	Gly	Ala	Pro
		835					840					845			
Ile	Gly	Ser	Gly	Ser	Ser	Asp	Ser	Ser	Met	Leu	Asp	Ser	Ala	Thr	Ser
	850					855					860				
Leu	Ile	Gln	Ala	Ala	Lys	Asn	Leu	Met	Asn	Ala	Val	Val	Leu	Thr	Val
865					870					875					880
Lys	Ala	Ser	Tyr	Val	Ala	Ser	Thr	Lys	Tyr	Gln	Lys	Val	Tyr	Gly	Thr

885 890 895
 Ala Ala Val Asn Ser Pro Val Val Ser Trp Lys Met Lys Ala Pro Glu
 900 905 910
 Lys Lys Pro Leu Val Lys Arg Glu Lys Pro Glu Glu Phe Gln Thr Arg
 915 920 925
 Val Arg Arg Gly Ser Gln Lys Lys His Ile Ser Pro Val Gln Ala Leu
 930 935 940
 Ser Glu Phe Lys Ala Met Asp Ser Phe
 945 950

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 <213> Homo sapiens

<220>
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 <223> beta-Catenin, Swissprot Accession P35222

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Met Ala Thr Gln Ala Asp Leu Met Glu Leu Asp Met Ala Met Glu Pro
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 Asp Arg Lys Ala Ala Val Ser His Trp Gln Gln Gln Ser Tyr Leu Asp
 20 25 30
 Ser Gly Ile His Ser Gly Ala Thr Thr Thr Ala Pro Ser Leu Ser Gly
 35 40 45
 Lys Gly Asn Pro Glu Glu Glu Asp Val Asp Thr Ser Gln Val Leu Tyr
 50 55 60
 Glu Trp Glu Gln Gly Phe Ser Gln Ser Phe Thr Gln Glu Gln Val Ala
 65 70 75 80
 Asp Ile Asp Gly Gln Tyr Ala Met Thr Arg Ala Gln Arg Val Arg Ala
 85 90 95
 Ala Met Phe Pro Glu Thr Leu Asp Glu Gly Met Gln Ile Pro Ser Thr
 100 105 110
 Gln Phe Asp Ala Ala His Pro Thr Asn Val Gln Arg Leu Ala Glu Pro
 115 120 125

Ser Gln Met Leu Lys His Ala Val Val Asn Leu Ile Asn Tyr Gln Asp
 130 135 140

Asp Ala Glu Leu Ala Thr Arg Ala Ile Pro Glu Leu Thr Lys Leu Leu
 145 150 155 160

Asn Asp Glu Asp Gln Val Val Val Asn Lys Ala Ala Val Met Val His
 165 170 175

Gln Leu Ser Lys Lys Glu Ala Ser Arg His Ala Ile Met Arg Ser Pro
 180 185 190

Gln Met Val Ser Ala Ile Val Arg Thr Met Gln Asn Thr Asn Asp Val
 195 200 205

Glu Thr Ala Arg Cys Thr Ala Gly Thr Leu His Asn Leu Ser His His
 210 215 220

Arg Glu Gly Leu Leu Ala Ile Phe Lys Ser Gly Gly Ile Pro Ala Leu
 225 230 235 240

Val Lys Met Leu Gly Ser Pro Val Asp Ser Val Leu Phe Tyr Ala Ile
 245 250 255

Thr Thr Leu His Asn Leu Leu Leu His Gln Glu Gly Ala Lys Met Ala
 260 265 270

Val Arg Leu Ala Gly Gly Leu Gln Lys Met Val Ala Leu Leu Asn Lys
 275 280 285

Thr Asn Val Lys Phe Leu Ala Ile Thr Thr Asp Cys Leu Gln Ile Leu
 290 295 300

Ala Tyr Gly Asn Gln Glu Ser Lys Leu Ile Ile Leu Ala Ser Gly Gly
 305 310 315 320

Pro Gln Ala Leu Val Asn Ile Met Arg Thr Tyr Thr Tyr Glu Lys Leu
 325 330 335

Leu Trp Thr Thr Ser Arg Val Leu Lys Val Leu Ser Val Cys Ser Ser
 340 345 350

Asn Lys Pro Ala Ile Val Glu Ala Gly Gly Met Gln Ala Leu Gly Leu
 355 360 365

His Leu Thr Asp Pro Ser Gln Arg Leu Val Gln Asn Cys Leu Trp Thr
 370 375 380

Leu Arg Asn Leu Ser Asp Ala Ala Thr Lys Gln Glu Gly Met Glu Gly
 385 390 400

Leu Leu Gly Thr Leu Val Gln Leu Leu Gly Ser Asp Asp Ile Asn Val
 405 410 415

Val Thr Cys Ala Ala Gly Ile Leu Ser Asn Leu Thr Cys Asn Asn Tyr
 420 425 430

Lys Asn Lys Met Met Val Cys Gln Val Gly Gly Ile Glu Ala Leu Val
 435 440 445

Arg Thr Val Leu Arg Ala Gly Asp Arg Glu Asp Ile Thr Glu Pro Ala
 450 455 460

Ile Cys Ala Leu Arg His Leu Thr Ser Arg His Gln Glu Ala Glu Met
 465 470 475 480

Ala Gln Asn Ala Val Arg Leu His Tyr Gly Leu Pro Val Val Val Lys
 485 490 495

Leu Leu His Pro Pro Ser His Trp Pro Leu Ile Lys Ala Thr Val Gly
 500 505 510

Leu Ile Arg Asn Leu Ala Leu Cys Pro Ala Asn His Ala Pro Leu Arg
 515 520 525

Glu Gln Gly Ala Ile Pro Arg Leu Val Gln Leu Leu Val Arg Ala His
 530 535 540

Gln Asp Thr Gln Arg Arg Thr Ser Met Gly Gly Thr Gln Gln Gln Phe
 545 550 555 560

Val Glu Gly Val Arg Met Glu Glu Ile Val Glu Gly Cys Thr Gly Ala
 565 570 575

Leu His Ile Leu Ala Arg Asp Val His Asn Arg Ile Val Ile Arg Gly
 580 585 590

Leu Asn Thr Ile Pro Leu Phe Val Gln Leu Leu Tyr Ser Pro Ile Glu
 595 600 605

Asn Ile Gln Arg Val Ala Ala Gly Val Leu Cys Glu Leu Ala Gln Asp
 610 615 620

Lys Glu Ala Ala Glu Ala Ile Glu Ala Glu Gly Ala Thr Ala Pro Leu
 625 630 635 640

Thr Glu Leu Leu His Ser Arg Asn Glu Gly Val Ala Thr Tyr Ala Ala
645 650 655

Ala Val Leu Phe Arg Met Ser Glu Asp Lys Pro Gln Asp Tyr Lys Lys
660 665 670

Arg Leu Ser Val Glu Leu Thr Ser Ser Leu Phe Arg Thr Glu Pro Met
675 680 685

Ala Trp Asn Glu Thr Ala Asp Leu Gly Leu Asp Ile Gly Ala Gln Gly
690 695 700

Glu Pro Leu Gly Tyr Arg Gln Asp Asp Pro Ser Tyr Arg Ser Phe His
705 710 715 720

Ser Gly Gly Tyr Gly Gln Asp Ala Leu Gly Met Asp Pro Met Met Glu
725 730 735

His Glu Met Gly Gly His His Pro Gly Ala Asp Tyr Pro Val Asp Gly
740 745 750

Leu Pro Asp Leu Gly His Ala Gln Asp Leu Met Asp Gly Leu Pro Pro
755 760 765

Gly Asp Ser Asn Gln Leu Ala Trp Phe Asp Thr Asp Leu
770 775 780

<210> 7
<211> 585
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(585)
<223> Involucrin, Swissprot Accession P07476

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Met Ser Gln Gln His Thr Leu Pro Val Thr Leu Ser Pro Ala Leu Ser
1 5 10 15

Gln Glu Leu Leu Lys Thr Val Pro Pro Val Asn Thr His Gln Glu
20 25 30

Gln Met Lys Gln Pro Thr Pro Leu Pro Pro Pro Cys Gln Lys Val Pro
35 40 45

Val Glu Leu Pro Val Glu Val Pro Ser Lys Gln Glu Glu Lys His Met
50 55 60

Thr Ala Val Lys Gly Leu Pro Glu Gln Glu Cys Glu Gln Gln Gln Lys
 65 70 75 80
 Glu Pro Gln Glu Gln Glu Leu Gln Gln Gln His Trp Glu Gln His Glu
 85 90 95
 Glu Tyr Gln Lys Ala Glu Asn Pro Glu Gln Gln Leu Lys Gln Glu Lys
 100 105 110
 Thr Gln Arg Asp Gln Gln Leu Asn Lys Gln Leu Glu Glu Glu Lys Lys
 115 120 125
 Leu Leu Asp Gln Gln Leu Asp Gln Glu Leu Val Lys Arg Asp Glu Gln
 130 135 140
 Leu Gly Met Lys Lys Glu Gln Leu Leu Glu Leu Pro Glu Gln Gln Glu
 145 150 155 160
 Gly His Leu Lys His Leu Glu Gln Gln Glu Gly Gln Leu Lys His Pro
 165 170 175
 Glu Gln Gln Glu Gly Gln Leu Glu Leu Pro Glu Gln Gln Glu Gly Gln
 180 185 190
 Leu Glu Leu Pro Glu Gln Gln Glu Gly Gln Leu Glu Leu Pro Glu Gln
 195 200 205
 Gln Glu Gly Gln Leu Glu Leu Pro Glu Gln Gln Glu Gly Gln Leu Glu
 210 215 220
 Leu Pro Gln Gln Gln Glu Gly Gln Leu Glu Leu Ser Glu Gln Gln Glu
 225 230 235 240
 Gly Gln Leu Glu Leu Ser Glu Gln Gln Glu Gly Gln Leu Glu Leu Ser
 245 250 255
 Glu Gln Gln Glu Gly Gln Leu Lys His Leu Glu His Gln Glu Gly Gln
 260 265 270
 Leu Glu Val Pro Glu Glu Gln Met Gly Gln Leu Lys Tyr Leu Glu Gln
 275 280 285
 Gln Glu Gly Gln Leu Lys His Leu Asp Gln Gln Glu Lys Gln Pro Glu
 290 295 300
 Leu Pro Glu Gln Gln Met Gly Gln Leu Lys His Leu Glu Gln Gln Glu
 305 310 315 320

Gly Gln Pro Lys His₃₂₅ Leu Glu Gln Gln Glu₃₃₀ Gly Gln Leu Glu Gln₃₃₅ Leu
 Glu Glu Gln Glu₃₄₀ Gly Gln Leu Lys His₃₄₅ Leu Glu Gln Gln Glu₃₅₀ Gly Gln
 Leu Glu His₃₅₅ Leu Glu His Gln Glu₃₆₀ Gly Gln Leu Gly Leu₃₆₅ Pro Glu Gln
 Gln Val₃₇₀ Leu Gln Leu Lys Gln₃₇₅ Leu Glu Lys Gln Gln₃₈₀ Gly Gln Pro Lys
 His₃₈₅ Leu Glu Glu Glu Glu₃₉₀ Gly Gln Leu Lys His₃₉₅ Leu Val Gln Gln Glu₄₀₀
 Gly Gln Leu Lys His₄₀₅ Leu Val Gln Gln Glu₄₁₀ Gly Gln Leu Glu Gln₄₁₅ Gln
 Glu Arg Gln Val₄₂₀ Glu His Leu Glu Gln₄₂₅ Gln Val Gly Gln Leu₄₃₀ Lys His
 Leu Glu Glu₄₃₅ Gln Glu Gly Gln Leu₄₄₀ Lys His Leu Glu Gln₄₄₅ Gln Gln Gly
 Gln Leu Glu Val Pro Glu Gln₄₅₅ Gln Val Gly Gln Pro₄₆₀ Lys Asn Leu Glu
 Gln₄₆₅ Glu Glu Lys Gln Leu₄₇₀ Glu Leu Pro Glu Gln₄₇₅ Gln Glu Gly Gln Val₄₈₀
 Lys His Leu Glu Lys₄₈₅ Gln Glu Ala Gln Leu₄₉₀ Glu Leu Pro Glu Gln₄₉₅ Gln
 Val Gly Gln Pro₅₀₀ Lys His Leu Glu Gln₅₀₅ Gln Glu Lys His Leu₅₁₀ Glu His
 Pro Glu Gln₅₁₅ Gln Asp Gly Gln Leu₅₂₀ Lys His Leu Glu Gln₅₂₅ Gln Glu Gly
 Gln Leu₅₃₀ Lys Asp Leu Glu Gln₅₃₅ Gln Lys Gly Gln Leu₅₄₀ Glu Gln Pro Val
 Phe₅₄₅ Ala Pro Ala Pro Gly₅₅₀ Gln Val Gln Asp Ile₅₅₅ Gln Pro Ala Leu₅₆₀ Pro
 Thr Lys Gly Glu Val₅₆₅ Leu Leu Pro Val Glu₅₇₀ His Gln Gln Gln Lys₅₇₅ Gln

Glu Val Gln Trp Pro Pro Lys His Lys
580 585

<210> 8
<211> 483
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(483)
<223> CK8, Swissprot Accession NP_002264

<400> 8

Met Ser Ile Arg Val Thr Gln Lys Ser Tyr Lys Val Ser Thr Ser Gly
1 5 10 15

Pro Arg Ala Phe Ser Ser Arg Ser Tyr Thr Ser Gly Pro Gly Ser Arg
20 25 30

Ile Ser Ser Ser Ser Phe Ser Arg Val Gly Ser Ser Asn Phe Arg Gly
35 40 45

Gly Leu Gly Gly Gly Tyr Gly Gly Ala Ser Gly Met Gly Gly Ile Thr
50 55 60

Ala Val Thr Val Asn Gln Ser Leu Leu Ser Pro Leu Val Leu Glu Val
65 70 75 80

Asp Pro Asn Ile Gln Ala Val Arg Thr Gln Glu Lys Glu Gln Ile Lys
85 90 95

Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu
100 105 110

Glu Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Gln
115 120 125

Gln Lys Thr Ala Arg Ser Asn Met Asp Asn Met Phe Glu Ser Tyr Ile
130 135 140

Asn Asn Leu Arg Arg Gln Leu Glu Thr Leu Gly Gln Glu Lys Leu Lys
145 150 155 160

Leu Glu Ala Glu Leu Gly Asn Met Gln Gly Leu Val Glu Asp Phe Lys
165 170 175

Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg Thr Glu Met Glu Asn Glu
180 185 190

Phe Val Leu Ile Lys Lys Asp Val Asp Glu Ala Tyr Met Asn Lys Val
195 200 205

Glu Leu Glu Ser Arg Leu Glu Gly Leu Thr Asp Glu Ile Asn Phe Leu
210 215 220

Arg Gln Leu Tyr Glu Glu Glu Ile Arg Glu Leu Gln Ser Gln Ile Ser
225 230 235 240

Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp Met
245 250 255

Asp Ser Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Asp Ile Ala Asn
260 265 270

Arg Ser Arg Ala Glu Ala Glu Ser Met Tyr Gln Ile Lys Tyr Glu Glu
275 280 285

Leu Gln Ser Leu Ala Gly Lys His Gly Asp Asp Leu Arg Arg Thr Lys
290 295 300

Thr Glu Ile Ser Glu Met Asn Arg Asn Ile Ser Arg Leu Gln Ala Glu
305 310 315 320

Ile Glu Gly Leu Lys Gly Gln Arg Ala Ser Leu Glu Ala Ala Ile Ala
325 330 335

Asp Ala Glu Gln Arg Gly Glu Leu Ala Ile Lys Asp Ala Asn Ala Lys
340 345 350

Leu Ser Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met Ala
355 360 365

Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Asn Val Lys Leu Ala Leu
370 375 380

Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser
385 390 395 400

Arg Leu Glu Ser Gly Met Gln Asn Met Ser Ile His Thr Lys Thr Thr
405 410 415

Ser Gly Tyr Ala Gly Gly Leu Ser Ser Ala Tyr Gly Gly Leu Thr Ser
420 425 430

Pro Gly Leu Ser Tyr Ser Leu Gly Ser Ser Phe Gly Ser Gly Ala Gly
435 440 445

Ser Ser Ser Phe Ser Arg Thr Ser Ser Ser Arg Ala Val Val Val Lys
450 455 460

Lys Ile Glu Thr Arg Asp Gly Lys Leu Val Ser Glu Ser Ser Asp Val
465 470 475 480

Leu Pro Lys

<210> 9
<211> 430
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(423)
<223> CK18, Swissprot Accession NP_954657

<400> 9

Met Ser Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu
1 5 10 15

Gly Ser Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala
20 25 30

Ala Ser Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val
35 40 45

Ser Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala
50 55 60

Thr Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu
65 70 75 80

Lys Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp
85 90 95

Arg Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile
100 105 110

Arg Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His
115 120 125

Tyr Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr
130 135 140

Val Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala
Page 25

145		150		155		160
Ala	Asp	Asp	Phe	Arg 165	Val	Lys
					Tyr	Glu
					Thr	Glu
					Leu	Ala
					Met	Arg
					Gln	
Ser	Val	Glu	Asn 180	Asp	Ile	His
					Gly	Leu
					Arg	Lys
					Val	Ile
					Asp	Asp
					Thr	
Asn	Ile	Thr 195	Arg	Leu	Gln	Leu
					Glu	Thr
					Glu	Ile
					Glu	Ala
					Leu	Lys
					Glu	
Glu	Leu 210	Leu	Phe	Met	Lys	Lys
					Asn	His
					Glu	Glu
					Glu	Val
					Lys	Gly
					Leu	
Gln	Ala	Gln	Ile	Ala	Ser 230	Ser
225					Gly	Leu
					Thr	Val
					Glu	Val
					Asp	Ala
					Pro	
240						
Lys	Ser	Gln	Asp	Leu 245	Ala	Lys
					Ile	Met
					Ala	Asp
					Ile	Arg
					Ala	Gln
					Tyr	
255						
Asp	Glu	Leu	Ala 260	Arg	Lys	Asn
					Arg	Glu
					Glu	Leu
					Asp	Lys
					Tyr	Trp
					Ser	
270						
Gln	Gln	Ile 275	Glu	Glu	Ser	Thr
					Thr	Val
					Val	Val
					Thr	Thr
					Gln	Ser
					Ala	Glu
285						
Val	Gly 290	Ala	Ala	Glu	Thr	Thr
					Leu	Thr
					Glu	Leu
					Arg	Arg
					Thr	Val
					Gln	
300						
Ser	Leu	Glu	Ile	Asp	Leu 310	Asp
305					Ser	Met
					Arg	Asn
					Leu	Lys
					Ala	Ser
					Leu	
320						
Glu	Asn	Ser	Leu	Arg 325	Glu	Val
					Glu	Ala
					Arg	Tyr
					Ala	Leu
					Gln	Met
					Glu	
335						
Gln	Leu	Asn	Gly 340	Ile	Leu	Leu
					His	Leu
					Glu	Ser
					Glu	Leu
					Ala	Gln
					Thr	
350						
Arg	Ala	Glu	Gly	Gln	Arg	Gln
					Ala	Gln
					Glu	Tyr
					Glu	Ala
					Leu	Leu
					Asn	
365						
Ile	Lys 370	Val	Lys	Leu	Glu	Ala
					Glu	Ile
					Ala	Thr
					Tyr	Arg
					Arg	Arg
					Leu	Leu
380						
Glu	Asp	Gly	Glu	Asp	Phe 390	Asn
385					Leu	Gly
					Asp	Ala
					Leu	Asp
					Ser	Ser
					Asn	
400						
Ser	Met	Gln	Thr	Ile	Gln	Lys
					Thr	Thr
					Thr	Arg
					Arg	Ile
					Val	Asp
					Gly	

405 410 415

Lys Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His
420 425 430

<210> 10
<211> 593
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(584)
<223> CK10, Swissprot Accession P13645

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Met Ser Val Arg Tyr Ser Ser Ser Lys His Tyr Ser Ser Ser Arg Ser
1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Gly Cys Gly Gly Gly Gly Gly Val Ser
20 25 30

Ser Leu Arg Ile Ser Ser Ser Lys Gly Ser Leu Gly Gly Gly Phe Ser
35 40 45

Ser Gly Gly Phe Ser Gly Gly Ser Phe Ser Arg Gly Ser Ser Gly Gly
50 55 60

Gly Cys Phe Gly Gly Ser Ser Gly Gly Tyr Gly Gly Leu Gly Gly Phe
65 70 75 80

Gly Gly Gly Ser Phe Arg Gly Ser Tyr Gly Ser Ser Ser Phe Gly Gly
85 90 95

Ser Tyr Gly Gly Ser Phe Gly Gly Gly Ser Phe Gly Gly Gly Ser Phe
100 105 110

Gly Gly Gly Ser Phe Gly Gly Gly Gly Phe Gly Gly Gly Gly Phe Gly
115 120 125

Gly Gly Phe Gly Gly Gly Phe Gly Gly Asp Gly Gly Leu Leu Ser Gly
130 135 140

Asn Glu Lys Val Thr Met Gln Asn Leu Asn Asp Arg Leu Ala Ser Tyr
145 150 155 160

Leu Asp Lys Val Arg Ala Leu Glu Glu Ser Asn Tyr Glu Leu Glu Gly
165 170 175

Lys Ile Lys Glu Trp Tyr Glu Lys His Gly Asn Ser His Gln Gly Glu
 180 185 190

Pro Arg Asp Tyr Ser Lys Tyr Tyr Lys Thr Ile Asp Asp Leu Lys Asn
 195 200 205

Gln Ile Leu Asn Leu Thr Thr Asp Asn Ala Asn Ile Leu Leu Gln Ile
 210 215 220

Asp Asn Ala Arg Leu Ala Ala Asp Asp Phe Arg Leu Lys Tyr Glu Asn
 225 230 235 240

Glu Val Ala Leu Arg Gln Ser Val Glu Ala Asp Ile Asn Gly Leu Arg
 245 250 255

Arg Val Leu Asp Glu Leu Thr Leu Thr Lys Ala Asp Leu Glu Met Gln
 260 265 270

Ile Glu Ser Leu Thr Glu Glu Leu Ala Tyr Leu Lys Lys Asn His Glu
 275 280 285

Glu Glu Met Lys Asp Leu Arg Asn Val Ser Thr Gly Asp Val Asn Val
 290 295 300

Glu Met Asn Ala Ala Pro Gly Val Asp Leu Thr Gln Leu Leu Asn Asn
 305 310 315 320

Met Arg Ser Gln Tyr Glu Gln Leu Ala Glu Gln Asn Arg Lys Asp Ala
 325 330 335

Glu Ala Trp Phe Asn Glu Lys Ser Lys Glu Leu Thr Thr Glu Ile Asp
 340 345 350

Asn Asn Ile Glu Gln Ile Ser Ser Tyr Lys Ser Glu Ile Thr Glu Leu
 355 360 365

Arg Arg Asn Val Gln Ala Leu Glu Ile Glu Leu Gln Ser Gln Leu Ala
 370 375 380

Leu Lys Gln Ser Leu Glu Ala Ser Leu Ala Glu Thr Glu Gly Arg Tyr
 385 390 395 400

Cys Val Gln Leu Ser Gln Ile Gln Ala Gln Ile Ser Ala Leu Glu Glu
 405 410 415

Gln Leu Gln Gln Ile Arg Ala Glu Thr Glu Cys Gln Asn Thr Glu Tyr
 420 425 430

Gln Gln Leu₄₃₅ Leu Asp Ile Lys₄₄₀ Ile Arg Leu Glu Asn₄₄₅ Glu Ile Gln Thr
 Tyr Arg₄₅₀ Ser Leu Leu Glu₄₅₅ Glu Gly Ser Ser₄₆₀ Gly Gly Gly Gly Arg
 Gly₄₆₅ Gly Gly Ser Phe₄₇₀ Gly Gly Gly Tyr Gly₄₇₅ Gly Ser Ser Gly₄₈₀
 Gly Ser Ser Gly₄₈₅ Gly Gly Tyr Gly Gly₄₉₀ His Gly Gly Ser₄₉₅ Ser Gly
 Gly Gly Tyr₅₀₀ Gly Gly Gly Ser Ser₅₀₅ Gly Gly Gly Ser Ser₅₁₀ Gly Gly
 Tyr Gly₅₁₅ Gly Ser Ser Ser₅₂₀ Gly Gly His Gly Gly₅₂₅ Ser Ser Ser
 Gly₅₃₀ Gly His Gly Gly Ser₅₃₅ Ser Ser Gly Gly Tyr₅₄₀ Gly Gly Ser Ser
 Gly₅₄₅ Gly Gly Gly Gly₅₅₀ Tyr Gly Gly Gly₅₅₅ Ser Ser Gly Gly Gly₅₆₀
 Ser Ser Gly Gly₅₆₅ Tyr Gly Gly Gly₅₇₀ Ser Ser Ser Gly Gly₅₇₅ His Lys
 Ser Ser Ser₅₈₀ Ser Gly Ser Val Gly₅₈₅ Glu Ser Ser Ser Lys₅₉₀ Gly Pro Arg

Tyr

<210> 11
 <211> 458
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(458)
 <223> CK13, Isoform a, Swissprot Accession NP_705694

<400> 11

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 Gly Gly Gly Ser₂₀ Cys Gln Leu Gly₂₅ Gly Arg Gly Val₃₀ Thr Cys

Ser Thr Arg Phe Val Ser Gly Gly Ser Ala Gly Gly Tyr Gly Gly Gly
 35 40 45
 Val Ser Cys Gly Phe Gly Gly Gly Ala Gly Ser Gly Phe Gly Gly Gly
 50 55 60
 Tyr Gly Gly Gly Leu Gly Gly Gly Tyr Gly Gly Gly Leu Gly Gly Gly
 65 70 75 80
 Phe Gly Gly Gly Phe Ala Gly Gly Phe Val Asp Phe Gly Ala Cys Asp
 85 90 95
 Gly Gly Leu Leu Thr Gly Asn Glu Lys Ile Thr Met Gln Asn Leu Asn
 100 105 110
 Asp Arg Leu Ala Ser Tyr Leu Glu Lys Val Arg Ala Leu Glu Glu Ala
 115 120 125
 Asn Ala Asp Leu Glu Val Lys Ile Arg Asp Trp His Leu Lys Gln Ser
 130 135 140
 Pro Ala Ser Pro Glu Arg Asp Tyr Ser Pro Tyr Tyr Lys Thr Ile Glu
 145 150 155 160
 Glu Leu Arg Asp Lys Ile Leu Thr Ala Thr Ile Glu Asn Asn Arg Val
 165 170 175
 Ile Leu Glu Ile Asp Asn Ala Arg Leu Ala Ala Asp Asp Phe Arg Leu
 180 185 190
 Lys Tyr Glu Asn Glu Leu Ala Leu Arg Gln Ser Val Glu Ala Asp Ile
 195 200 205
 Asn Gly Leu Arg Arg Val Leu Asp Glu Leu Thr Leu Ser Lys Thr Asp
 210 215 220
 Leu Glu Met Gln Ile Glu Ser Leu Asn Glu Glu Leu Ala Tyr Met Lys
 225 230 235 240
 Lys Asn His Glu Glu Glu Met Lys Glu Phe Ser Asn Gln Val Val Gly
 245 250 255
 Gln Val Asn Val Glu Met Asp Ala Thr Pro Gly Ile Asp Leu Thr Arg
 260 265 270
 Val Leu Ala Glu Met Arg Glu Gln Tyr Glu Ala Met Ala Glu Arg Asn
 275 280 285

Arg Arg Asp Ala Glu Glu Trp Phe His Ala Lys Ser Ala Glu Leu Asn
290 295 300

Lys Glu Val Ser Thr Asn Thr Ala Met Ile Gln Thr Ser Lys Thr Glu
305 310 315 320

Ile Thr Glu Leu Arg Arg Thr Leu Gln Gly Leu Glu Ile Glu Leu Gln
325 330 335

Ser Gln Leu Ser Met Lys Ala Gly Leu Glu Asn Thr Val Ala Glu Thr
340 345 350

Glu Cys Arg Tyr Ala Leu Gln Leu Gln Gln Ile Gln Gly Leu Ile Ser
355 360 365

Ser Ile Glu Ala Gln Leu Ser Glu Leu Arg Ser Glu Met Glu Cys Gln
370 375 380

Asn Gln Glu Tyr Lys Met Leu Leu Asp Ile Lys Thr Arg Leu Glu Gln
385 390 395 400

Glu Ile Ala Thr Tyr Arg Ser Leu Leu Glu Gly Gln Asp Ala Lys Met
405 410 415

Ile Gly Phe Pro Ser Ser Ala Gly Ser Val Ser Pro Arg Ser Thr Ser
420 425 430

Val Thr Thr Thr Ser Ser Ala Ser Val Thr Thr Thr Ser Asn Ala Ser
435 440 445

Gly Arg Arg Thr Ser Asp Val Arg Arg Pro
450 455

<210> 12
<211> 968
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(968)
<223> p120, Swissprot Accession O60716

<400> 12

Met Asp Asp Ser Glu Val Glu Ser Thr Ala Ser Ile Leu Ala Ser Val
1 5 10 15

Lys Glu Gln Glu Ala Gln Phe Glu Lys Leu Thr Arg Ala Leu Glu Glu
20 25 30

Glu Arg Arg His Val Ser Ala Gln Leu Glu Arg Val Arg Val Ser Pro
 35 40 45
 Gln Asp Ala Asn Pro Leu Met Ala Asn Gly Thr Leu Thr Arg Arg His
 50 55 60
 Gln Asn Gly Arg Phe Val Gly Asp Ala Asp Leu Glu Arg Gln Lys Phe
 65 70 75 80
 Ser Asp Leu Lys Leu Asn Gly Pro Gln Asp His Ser His Leu Leu Tyr
 85 90 95
 Ser Thr Ile Pro Arg Met Gln Glu Pro Gly Gln Ile Val Glu Thr Tyr
 100 105 110
 Thr Glu Glu Asp Pro Glu Gly Ala Met Ser Val Val Ser Val Glu Thr
 115 120 125
 Ser Asp Asp Gly Thr Thr Arg Arg Thr Glu Thr Thr Val Lys Lys Val
 130 135 140
 Val Lys Thr Val Thr Thr Arg Thr Val Gln Pro Val Ala Met Gly Pro
 145 150 155 160
 Asp Gly Leu Pro Val Asp Ala Ser Ser Val Ser Asn Asn Tyr Ile Gln
 165 170 175
 Thr Leu Gly Arg Asp Phe Arg Lys Asn Gly Asn Gly Gly Pro Gly Pro
 180 185 190
 Tyr Val Gly Gln Ala Gly Thr Ala Thr Leu Pro Arg Asn Phe His Tyr
 195 200 205
 Pro Pro Asp Gly Tyr Ser Arg His Tyr Glu Asp Gly Tyr Pro Gly Gly
 210 215 220
 Ser Asp Asn Tyr Gly Ser Leu Ser Arg Val Thr Arg Ile Glu Glu Arg
 225 230 235 240
 Tyr Arg Pro Ser Met Glu Gly Tyr Arg Ala Pro Ser Arg Gln Asp Val
 245 250 255
 Tyr Gly Pro Gln Pro Gln Val Arg Val Gly Gly Ser Ser Val Asp Leu
 260 265 270
 His Arg Phe His Pro Glu Pro Tyr Gly Leu Glu Asp Asp Gln Arg Ser
 275 280 285

Met Gly Tyr Asp Asp Leu Asp Tyr Gly Met Met Ser Asp Tyr Gly Thr
290 295 300
Ala Arg Arg Thr Gly Thr Pro Ser Asp Pro Arg Arg Arg Leu Arg Ser
305 310 315 320
Tyr Glu Asp Met Ile Gly Glu Glu Val Pro Ser Asp Gln Tyr Tyr Trp
325 330 335
Ala Pro Leu Ala Gln His Glu Arg Gly Ser Leu Ala Ser Leu Asp Ser
340 345 350
Leu Arg Lys Gly Gly Pro Pro Pro Pro Asn Trp Arg Gln Pro Glu Leu
355 360 365
Pro Glu Val Ile Ala Met Leu Gly Phe Arg Leu Asp Ala Val Lys Ser
370 375 380
Asn Ala Ala Ala Tyr Leu Gln His Leu Cys Tyr Arg Asn Asp Lys Val
385 390 395 400
Lys Thr Asp Val Arg Lys Leu Lys Gly Ile Pro Val Leu Val Gly Leu
405 410 415
Leu Asp His Pro Lys Lys Glu Val His Leu Gly Ala Cys Gly Ala Leu
420 425 430
Lys Asn Ile Ser Phe Gly Arg Asp Gln Asp Asn Lys Ile Ala Ile Lys
435 440 445
Asn Cys Asp Gly Val Pro Ala Leu Val Arg Leu Leu Arg Lys Ala Arg
450 455 460
Asp Met Asp Leu Thr Glu Val Ile Thr Gly Thr Leu Trp Asn Leu Ser
465 470 475 480
Ser His Asp Ser Ile Lys Met Glu Ile Val Asp His Ala Leu His Ala
485 490 495
Leu Thr Asp Glu Val Ile Ile Pro His Ser Gly Trp Glu Arg Glu Pro
500 505 510
Asn Glu Asp Cys Lys Pro Arg His Ile Glu Trp Glu Ser Val Leu Thr
515 520 525
Asn Thr Ala Gly Cys Leu Arg Asn Val Ser Ser Glu Arg Ser Glu Ala
530 535 540

Arg Arg Lys Leu Arg Glu Cys Asp Gly Leu Val Asp Ala Leu Ile Phe
 545 550 555 560
 Ile Val Gln Ala Glu Ile Gly Gln Lys Asp Ser Asp Ser Lys Leu Val
 565 570 575
 Glu Asn Cys Val Cys Leu Leu Arg Asn Leu Ser Tyr Gln Val His Arg
 580 585 590
 Glu Ile Pro Gln Ala Glu Arg Tyr Gln Glu Ala Ala Pro Asn Val Ala
 595 600 605
 Asn Asn Thr Gly Pro His Ala Ala Ser Cys Phe Gly Ala Lys Lys Gly
 610 615 620
 Lys Asp Glu Trp Phe Ser Arg Gly Lys Lys Pro Ile Glu Asp Pro Ala
 625 630 635 640
 Asn Asp Thr Val Asp Phe Pro Lys Arg Thr Ser Pro Ala Arg Gly Tyr
 645 650 655
 Glu Leu Leu Phe Gln Pro Glu Val Val Arg Ile Tyr Ile Ser Leu Leu
 660 665 670
 Lys Glu Ser Lys Thr Pro Ala Ile Leu Glu Ala Ser Ala Gly Ala Ile
 675 680 685
 Gln Asn Leu Cys Ala Gly Arg Trp Thr Tyr Gly Arg Tyr Ile Arg Ser
 690 695 700
 Ala Leu Arg Gln Glu Lys Ala Leu Ser Ala Ile Ala Asp Leu Leu Thr
 705 710 715 720
 Asn Glu His Glu Arg Val Val Lys Ala Ala Ser Gly Ala Leu Arg Asn
 725 730 735
 Leu Ala Val Asp Ala Arg Asn Lys Glu Leu Ile Gly Lys His Ala Ile
 740 745 750
 Pro Asn Leu Val Lys Asn Leu Pro Gly Gly Gln Gln Asn Ser Ser Trp
 755 760 765
 Asn Phe Ser Glu Asp Thr Val Ile Ser Ile Leu Asn Thr Ile Asn Glu
 770 775 780
 Val Ile Ala Glu Asn Leu Glu Ala Ala Lys Lys Leu Arg Glu Thr Gln
 785 790 795 800

Gly Ile Glu Lys Leu Val Leu Ile Asn Lys Ser Gly Asn Arg Ser Glu
805 810 815

Lys Glu Val Arg Ala Ala Ala Leu Val Leu Gln Thr Ile Trp Gly Tyr
820 825 830

Lys Glu Leu Arg Lys Pro Leu Glu Lys Glu Gly Trp Lys Lys Ser Asp
835 840 845

Phe Gln Val Asn Leu Asn Asn Ala Ser Arg Ser Gln Ser Ser His Ser
850 855 860

Tyr Asp Asp Ser Thr Leu Pro Leu Ile Asp Arg Asn Gln Lys Ser Asp
865 870 875 880

Lys Lys Pro Asp Arg Glu Glu Ile Gln Met Ser Asn Met Gly Ser Asn
885 890 895

Thr Lys Ser Leu Asp Asn Asn Tyr Ser Thr Pro Asn Glu Arg Gly Asp
900 905 910

His Asn Arg Thr Leu Asp Arg Ser Gly Asp Leu Gly Asp Met Glu Pro
915 920 925

Leu Lys Gly Thr Thr Pro Leu Met Gln Asp Glu Gly Gln Glu Ser Leu
930 935 940

Glu Glu Glu Leu Asp Val Leu Val Leu Asp Asp Glu Gly Gly Gln Val
945 950 955 960

Ser Tyr Pro Ser Met Gln Lys Ile
965

<210> 13
<211> 156
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(156)
<223> p16INK4a, Swissprot Accession P42771

<400> 13

Met Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1 5 10 15

Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
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20 25 30
 Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
 35 40 45
 Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
 50 55 60
 Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
 65 70 75 80
 Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
 85 90 95
 Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
 100 105 110
 Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
 115 120 125
 Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
 130 135 140
 Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
 145 150 155

<210> 14
 <211> 173
 <212> PRT
 <213> Homo sapiens

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 <222> (1)..(173)
 <223> p14arf, Swissprot Accession Q8N726

<400> 14

Met Gly Arg Gly Arg Cys Val Gly Pro Ser Leu Gln Leu Arg Gly Gln
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 Glu Trp Arg Cys Ser Pro Leu Val Pro Lys Gly Gly Ala Ala Ala Ala
 20 25 30
 Glu Leu Gly Pro Gly Gly Gly Glu Asn Met Val Arg Arg Phe Leu Val
 35 40 45
 Thr Leu Arg Ile Arg Arg Ala Cys Gly Pro Pro Arg Val Arg Val Phe
 50 55 60

Val Val His Ile Pro Arg Leu Thr Gly Glu Trp Ala Ala Pro Gly Ala
65 70 75 80
Pro Ala Ala Val Ala Leu Val Leu Met Leu Leu Arg Ser Gln Arg Leu
85 90 95
Gly Gln Gln Pro Leu Pro Arg Arg Pro Gly His Asp Asp Gly Gln Arg
100 105 110
Pro Ser Gly Gly Ala Ala Ala Ala Pro Arg Arg Gly Ala Gln Leu Arg
115 120 125
Arg Pro Arg His Ser His Pro Thr Arg Ala Arg Arg Cys Pro Gly Gly
130 135 140
Leu Pro Gly His Ala Gly Gly Ala Ala Pro Gly Arg Gly Ala Ala Gly
145 150 155 160
Arg Ala Arg Cys Leu Gly Pro Ser Ala Arg Gly Pro Gly
165 170